AUG 18 2004 S

Seq list.ST25.txt SEQUENCE LISTING

Valentis, Inc. Nordstrom, Jeff Freimark, Bruce Deshpande, Deepa

<120> Gene Expression and Delivery Systems and Uses

<130> 213-0063US

<140> US 09/754,014

<141> 2001-01-03

<150> US 08/948,958

<151> 1997-10-10

<150> US 60/028,687

· <151> 1996-10-10

<160> 19

<170> PatentIn version 3.3

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<212> PRT

<213> Homo sapiens

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Val Glu Leu Asp Trp Tyr Pro Asp Ala Pro Gly Glu Met Val Val Leu 35 40 45

Thr Cys Asp Thr Pro Glu Glu Asp Gly Ile Thr Trp Thr Leu Asp Gln 50 60

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys 65 70 75 80

Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val 85 90 95

Leu Ser His Ser Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp 100 105 110

Ser Thr Asp Ile Leu Lys Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe 115 120 125

Leu Arg Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp 130 135 140

Leu Thr Thr Ile Ser Thr Asp Leu Thr Phe Ser Val Lys Ser Ser Arg 145 150 155 160

Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser 165 170 175

Ala Glu Arg Val Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu
180 185 190

Cys Gln Glu Asp Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile 195 200 205

Glu Val Met Val Asp Ala Val His Lys Leu Lys Tyr Glu Asn Tyr Thr 210 215 220

Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn 225 230 235 240

Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser Trp
245 250 255

. Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr 260 265 270

Phe Cys Val Gln Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg 275 280 285

Val Phe Thr Asp Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn Ala 290 295 300

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Glu Trp Ala Ser Val Pro Cys Ser 325

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gctgctgagg	agagtctgcc	cattgaggtc	atggtggatg	ccgttcacaa	gctcaagtat	660
gaaaactaca	ccagcagctt	cttcatcagg	gacatcatca	aacctgaccc	acccaagaac	720
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	aaggagccca	agaacaagac	cttcctgcgc	tgcgaggcca	agaactacag	cggccgcttc	420
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	cgcggcgaca	acaaggagta	cgagtacagc	gtggagtgcc	aggaagactc	cgcctgcccc	600
	gccgctgagg	agagcctgcc	catcgaggtg	atggtggacg	ccgttcacaa	gctgaagtac	660
	gagaactaca	ccagcagctt	cttcatccgc	gacatcatca	agcctgaccc	acccaagaac	720
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840

900

960

987

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Gly Met Phe Pro Cys L	Leu His His Ser Gln Asn	Leu Leu Arg Ala Val						
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Ser Asn Met Leu Gln L	Lys Ala Arg Gln Thr Leu	Glu Phe Tyr Pro Cys						
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Thr Val Glu Ala Cys L	Leu Pro Leu Glu Leu Thr	Lys Asn Glu Ser Cys						
85	90	95						
Leu Asn Ser Arg Glu T	Thr Ser Phe Ile Thr Asn	Gly Ser Cys Leu Ala						
100	105	110						
Ser Arg Lys Thr Ser F	Phe Met Met Ala Leu Cys	Leu Ser Ser Ile Tyr						
115	120	125						
Glu Asp Leu Lys Met T	Tyr Gln Val Glu Phe Lys	Thr Met Asn Ala Lys						
130	135	140						
	Lys Arg Gln Ile Phe Leu 150 155	Asp Gln Asn Met Leu 160						
Ala Val Ile Asp Glu I	Leu Met Gln Ala Leu Asn	Phe Asn Ser Glu Thr						
165	170	175						

Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys 180 185 190

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Ile Asp Arg Val Thr Ser Tyr Leu Asn Ala Ser 210 215

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tcccaaaacc	tgctgagggc	cgtcagcaac	atgctccaga	aggccagaca	aactctagaa	180
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gagacctctt	tcataactaa	tgggagttgc	ctggcctcca	gaaagacctc	ttttatgatg	360
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gcagttattg	atgagctgat	gcaggccctg	aatttcaaca	gtgagactgt	gccacaaaaa	540
tectecettg	aagaaccgga	tttttataaa	actaaaatca	agctctgcat	acttcttcat	600
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agccagaacc tgctggcggc cgtgagcaac atgctgcaga aggccgcgca gaccctggag 180
ttctacccct gcaccagcga ggagatcgac cacgaggaca tcaccaagga caagaccagc 240
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	gagaccagct	tcatcaccaa	cggcagctgc	ctggccagcc	gcaagaccag	cttcatgatg	360
	gccctgtgcc	tgagcagcat	ctacgaggac	ctgaagatgt	accaggtgga	gttcaagacc	420
	atgaacgcca	agctgctgat	ggaccccaag	ctccagatct	tcctggacca	gaacatgctg	480
	gccgtgatcg	acgagctgat	gcaggccctg	aacttcaaca	gcgagaccgt	gccccagaag	540
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			cgtgagcaac				180
			ggagatcgac				240
			cctcgagtta				300
-	gagacctcct	tcatcaccaa	cggcacttgc	ctggcctccc	gcaagaccag	cttcatgatg	360
	gccctgtgcc	tgagctccat	ctacgaggac	ctgaagatgt	accaggtgga	gttcaagacc	420
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	gccttccgca	tccgggccgt	gaccatcgac	cgcgtgacca	gctacctgaa	cgccacgtga	660
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Seq list.ST25.txt
 <211>
        45
 <212> DNA
 <213> artificial sequence
 <220>
 <223> synthetic intron where tract of random nucleotides not shown
 <220>
       misc_feature
 <221>
 <222>
        (1)..(9)
 <223> 5' splice site, where actual splice between nucleotide 3 and 4
 <220>
 <221> misc_feature
 <222>
        (10)..(15)
 <223>
        optional restriction enzyme site
<220>
 <221>
       misc_feature
 <222>
        (15)..(16)
 <223> between 15 and 16 is the location of random sequence
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 <221> misc_feature
 <222>
        (16)..(22)
        branch point, where the actual branch point is nucleotide #21
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 <220>
 <221> misc_feature
 <222>
        (25)..(45)
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        44 and 45
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                                                                        45
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 <210> 11
 <211>
        16
 <212>
        DNA
 <213> Artificial
 <220>
 <223> consensus 3' intron splice site,
 <220>
 <221> misc_feature
 <222>
        (1)..(16)
        The letter "N" can be any base.
 <223>
 The letter "Y" can be C or T.
 <400> 11
                                                                        16
 ууууууууу улуадд
```

<210> 12

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<211> 271
<212> DNA
<213> artificial
<220>
<223> artificial Poly A site 2XPA
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                                                                  120
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                                                                  180
qtctctcact cggtactaga gcatttttcc ctctgccaaa aattatgggg acatcatgaa
                                                                  240
gccccttgag catctgacgt ctggctaata aaggaaattt attttcattg caatagtgtg
                                                                  271
ttggaatttt ttgtgtctct cactcggtac c
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      13
<211>
      122
<212>
      DNA
<213>
      artificial
<220>
<223> synthetic intron
<220>
<221> misc_feature
<222>
       (1)..(9)
<223>
      5' splice site, where the actual 5' splice site is between
       nucleotide 3 and 4
<220>
<221>
      misc_feature
<222>
       (10)..(15)
<223>
      optional restriction enzyme site
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<221>
      misc_feature
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       (16)..(92)
       "n" = random nucleotides, including optional restriction enzyme
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<220>
<221> misc_feature
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       (93)..(99)
      branch point, where the actual branch point is nucleotide #98
<223>
<220>
<221>
      misc_feature
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       (102)..(122)
       3' splice site, where the actual 3' splice site is between
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       nucleotides 121 and 122
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Seq list.ST25.txt
 nnnnnnnn nnnnnnnnn nnnnnnnnn nntactaacg gttcttttt tctcttcaca
                                                                      122
 gg
 <210> 14
 <211> 9
 <212> DNA
 <213> artificial
 <220>
 <223> consensus 5' splice site
 <220>
 <221> misc
 <222>
        (1)..(1)
 <223> The letter "m" stands for C or A.
 <220>
 <221> misc
<222>
        (3)..(4)
 <223> actual '5 splice site
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 <221>
       misc
 <222>
        (6)..(6)
 <223> The letter "R" stands for G or A
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                                                                        9
 maggtragt
° <210> 15
 <211>
        9
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        misc_feature
 <222>
        (3)..(4)
 <223> Actual splice site between nucleotides 3 and 4
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 caggtaagt
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        7
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        artificial
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 <223> consensus mammalian branch point
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        (1)..(7)
 <223> The letter "Y" stands for C or T.
        The letter "R" stands for A or G.
        The letter "N" stands for any base.
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 <221> misc_feature
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        (6)..(6)
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        7
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        DNA
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 <220>
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                                                                          7
 tactaac
 <210>
        18
 <211>
        21
• <212>
        DNA
        artificial
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<220>
 <223> 3' splice, with polypyrimidine tract extended to 16 bases
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        misc_feature
 <221>
 <222>
        (1)..(16)
 <223>
        The letter "Y" stands for C or T.
 <220>
        misc_feature
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        (17)..(17)
        The letter "N" stands for any base.
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        misc_feature
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        (18)..(18)
 <223>
        The letter "Y" stands for C or T.
 <220>
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        misc_feature
 <222>
        (20)..(21)
        Actual 5' splice site
 <223>
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	<400> УУУУУУ	18 уууу уууууулуад д	21
•			
	<210> <211>	21	
•	<212>	DNA artificial	
•	<220> <223>	OPTIVS8 3' splice site with 7 consecutive Ts	
-	<222>	<pre>misc_feature (17)(17) The letter "N" stands for any base.</pre>	
•	<222>	misc_feature (18)(18) The letter "Y" stands for C or T.	
	<400> ttcttt	19 tttt ctcttcnyag g	21